

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2006, 17:12:50 ; Search time 19405 Seconds
(without alignments)
19849.129 Million cell updates/sec

Title: US-10-804-772-1
Perfect score: 6888
Sequence: 1 atgtgggtattatattgttg.....cctagttcaggccaaagctt 6888

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			ID	Description
Result	No.	Score	Match	Length	DB			
c	1	744.4	10.8	900	13	CL514078		CL514078 SAIL_882
	2	727	10.6	1605	6	CNS0A4TW		BX824287 Arabidops
	3	695	10.1	1797	6	CNS0A70Q		BX822540 Arabidops

	4	541.4	7.9	543	11	B77695	B77695 T28K14TF TA
	5	534.2	7.8	563	14	BX292216	BX292216 Arabidops
	6	526.6	7.6	1038	4	BX839458	BX839458 BX839458
	7	485.4	7.0	651	7	AV824772	AV824772 AV824772
c	8	474	6.9	845	14	DU985218	DU985218 KBrH1076J
c	9	426.2	6.2	937	13	CL493476	CL493476 SAIL_580_
	10	401.2	5.8	457	14	CR397647	CR397647 Arabidops
	11	385.6	5.6	1397	14	AJ859443	AJ859443 Brassica
	12	372.8	5.4	460	14	CR397648	CR397648 Arabidops
c	13	359	5.2	434	3	BP606549	BP606549 BP606549
	14	355.6	5.2	375	12	CC797957	CC797957 SALK_1456
c	15	343.6	5.0	423	7	AV787618	AV787618 AV787618
c	16	337	4.9	951	13	CL516966	CL516966 SAIL_98_C
	17	333.4	4.8	698	5	CD814113	CD814113 BN15.022A
c	18	320	4.6	424	3	BP603351	BP603351 BP603351
c	19	320	4.6	446	3	BP612187	BP612187 BP612187
c	20	309.2	4.5	342	14	BX533508	BX533508 Arabidops
c	21	305.6	4.4	363	3	BP622314	BP622314 BP622314
	22	296	4.3	965	4	BX839894	BX839894 BX839894
c	23	291.8	4.2	908	13	CL516967	CL516967 SAIL_98_C
c	24	283	4.1	416	3	BP565879	BP565879 BP565879
c	25	283	4.1	417	3	BP563350	BP563350 BP563350
c	26	283	4.1	433	3	BP564785	BP564785 BP564785
c	27	272	3.9	414	3	BP575355	BP575355 BP575355
	28	270	3.9	364	3	BP803469	BP803469 BP803469
c	29	269.2	3.9	404	3	BP580791	BP580791 BP580791
c	30	266.6	3.9	273	11	BZ287389	BZ287389 SALK_0207
c	31	263	3.8	875	13	CL469983	CL469983 SAIL_136_
c	32	255.8	3.7	370	3	BP567237	BP567237 BP567237
	33	252.6	3.7	360	3	BP803450	BP803450 BP803450
c	34	251	3.6	442	3	BP577809	BP577809 BP577809
	35	234.2	3.4	923	13	CL502551	CL502551 SAIL_713_
c	36	209	3.0	788	11	BZ483015	BZ483015 BONNO30TR
	37	205.6	3.0	552	10	DT014799	DT014799 VVI092G03
	38	205.4	3.0	647	3	BU887383	BU887383 R058F09 P
	39	203.8	3.0	659	8	CX182444	CX182444 D12_45-46
	40	203.8	3.0	806	10	DT503533	DT503533 WS0136.BR
	41	203.4	3.0	943	10	DT568185	DT568185 EST107882
	42	202.8	2.9	753	10	DV134569	DV134569 CV03108B2
	43	201.2	2.9	602	10	DT013384	DT013384 VVH050E10
	44	201.2	2.9	645	10	DT014183	DT014183 VVH009D08
	45	199	2.9	490	10	DT009234	DT009234 VVH034D03

ALIGNMENTS

RESULT 1

CL514078/c

LOCUS CL514078 900 bp DNA linear GSS 01-APR-2004

DEFINITION SAIL_882_F07.v2 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_882_F07.v2, genomic survey sequence.

ACCESSION CL514078

VERSION CL514078.1 GI:46011398

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 31, 2006, 16:30:37 ; Search time 24949 Seconds
(without alignments)
17654.809 Million cell updates/sec

Title: US-10-804-772-1
Perfect score: 6888
Sequence: 1 atgtgggtattatattgttg.....cctagttcaggccaaagctt 6888

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			Description
Result	No.	Score	Match	Length	ID		
c	1	6753.6	98.0	84196	4	ATT3A5	AL132979 Arabidops
	2	4818	69.9	4818	4	AF044216	AF044216 Arabidops

	3	3379	49.1	3379	2	CS258467	CS258467 Sequence
	4	750.4	10.9	1691	4	AF412114	AF412114 Arabidops
	5	722.4	10.5	1542	4	AY090266	AY090266 Arabidops
	6	669	9.7	1035	2	CS258452	CS258452 Sequence
	7	384.6	5.6	121254	4	CT033768	CT033768 Medicago
	8	381.2	5.5	134939	4	AC147964	AC147964 Medicago
c	9	377	5.5	130026	12	AC174298	AC174298 Medicago
c	10	331.4	4.8	96298	12	AP007781	AP007781 Lotus cor
	11	205.2	3.0	1777	4	AB231155	AB231155 Zinnia el
	12	187.6	2.7	110000	4	AP008209_066	Continuation (67 o
	13	187.6	2.7	110000	4	AP008209_067	Continuation (68 o
	14	187.6	2.7	127946	4	AC104473	AC104473 Oryza sat
	15	176.8	2.6	191	7	AL844732	AL844732 Arabidops
c	16	140.4	2.0	8056	2	AX599046	AX599046 Sequence
	17	136.4	2.0	8056	2	AX599046	AX599046 Sequence
	18	135.6	2.0	6508	2	AR566958	AR566958 Sequence
	19	135.6	2.0	250029	13	AE014839	AE014839 Plasmodiu
	20	135	2.0	349751	13	PFMAL4P3	AL035476 Plasmodiu
	21	134	1.9	100269	4	ATF18022	AL163817 Arabidops
	22	133.2	1.9	104992	12	AC005504	AC005504 Plasmodiu
	23	133.2	1.9	169546	12	AC004157	AC004157 Plasmodiu
c	24	133.2	1.9	250421	13	AE014849	AE014849 Plasmodiu
	25	132.8	1.9	1509	2	CS258469	CS258469 Sequence
	26	132.8	1.9	1521	4	AB206579	AB206579 Oryza sat
c	27	130.8	1.9	104992	12	AC005504	AC005504 Plasmodiu
c	28	130.8	1.9	169546	12	AC004157	AC004157 Plasmodiu
	29	130.8	1.9	250421	13	AE014849	AE014849 Plasmodiu
	30	130.6	1.9	313050	13	PFA929352	AL929352 Plasmodiu
c	31	130.4	1.9	254050	13	PFA929358	AL929358 Plasmodiu
	32	129.4	1.9	14867	13	AE001398	AE001398 Plasmodiu
	33	128.6	1.9	172816	5	AC093899	AC093899 Homo sapi
	34	128	1.9	106142	4	AC025417	AC025417 Genomic s
	35	127.8	1.9	86826	13	PFMAL3P5	AL034556 Plasmodiu
c	36	126.4	1.8	133877	12	AC120883	AC120883 Homo sapi
c	37	125.4	1.8	86826	13	PFMAL3P5	AL034556 Plasmodiu
c	38	125.4	1.8	349751	13	PFMAL4P3	AL035476 Plasmodiu
c	39	124.6	1.8	205130	12	AC105425	AC105425 Homo sapi
	40	124.4	1.8	4601	13	DMU11584	U11584 Drosophila
	41	124.4	1.8	19517	13	DMU37541	U37541 Drosophila
c	42	124	1.8	8056	2	AX598900	AX598900 Sequence
c	43	123.4	1.8	67970	13	PFMAL1P3	AL031746 Plasmodiu
	44	123.2	1.8	8056	2	AX598900	AX598900 Sequence
	45	123.2	1.8	110000	12	TANN3_01	Continuation (2 of

ALIGNMENTS

RESULT 1

ATT3A5/c

LOCUS ATT3A5 84196 bp DNA linear PLN 16-APR-2005
 DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone T3A5.
 ACCESSION AL132979
 VERSION AL132979.2 GI:6782244
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 1, 2006, 05:51:05 ; Search time 804 Seconds
(without alignments)
16030.096 Million cell updates/sec

Title: US-10-804-772-1
Perfect score: 6888
Sequence: 1 atgtgggtattatattgttg.....cctagttcaggccaaagctt 6888

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	6888	100.0	6888	4 US-09-502-426B-1	Sequence 1, Appli
2	135.6	2.0	6508	3 US-09-995-917A-2	Sequence 2, Appli
3	94.6	1.4	1181	3 US-09-464-535-35	Sequence 3'5, Appl
4	92.8	1.3	4937	2 US-08-622-166A-3	Sequence 3, Appli
5	88.2	1.3	453	3 US-09-464-535-11	Sequence 11, Appli
6	87.6	1.3	1608	2 US-08-622-166A-1	Sequence 1, Appli
c 7	84	1.2	18773	3 US-09-949-016-14164	Sequence 14164, A

	8	82.8	1.2	436	3	US-09-464-535-13	Sequence 13, Appl
	9	82.8	1.2	600	3	US-09-464-535-39	Sequence 39, Appl
	10	82.4	1.2	1149	3	US-09-995-917A-3	Sequence 3, Appli
	11	82.4	1.2	18773	3	US-09-949-016-14164	Sequence 14164, A
c	12	80.8	1.2	187169	3	US-09-949-016-12776	Sequence 12776, A
c	13	80.8	1.2	191569	3	US-09-949-016-15940	Sequence 15940, A
c	14	80.8	1.2	205044	3	US-09-949-016-15851	Sequence 15851, A
c	15	80.8	1.2	205044	3	US-09-949-016-15852	Sequence 15852, A
c	16	80.8	1.2	205044	3	US-09-949-016-15853	Sequence 15853, A
c	17	80.8	1.2	223471	3	US-09-949-016-12387	Sequence 12387, A
c	18	80.8	1.2	223471	3	US-09-949-016-12724	Sequence 12724, A
c	19	80.8	1.2	223471	3	US-09-949-016-12725	Sequence 12725, A
c	20	80	1.2	134987	3	US-09-949-016-15348	Sequence 15348, A
c	21	80	1.2	134987	3	US-09-949-016-15349	Sequence 15349, A
c	22	80	1.2	134987	3	US-09-949-016-15350	Sequence 15350, A
c	23	80	1.2	134987	3	US-09-949-016-15507	Sequence 15507, A
c	24	80	1.2	134987	3	US-09-949-016-15508	Sequence 15508, A
c	25	80	1.2	134987	3	US-09-949-016-15509	Sequence 15509, A
	26	80	1.2	640681	3	US-09-790-988-1	Sequence 1, Appli
	27	79.8	1.2	12313	3	US-09-949-016-13248	Sequence 13248, A
	28	79.4	1.2	95255	3	US-09-949-016-17067	Sequence 17067, A
	29	79	1.1	25590	3	US-09-949-002-777	Sequence 777, App
	30	78.6	1.1	187169	3	US-09-949-016-12776	Sequence 12776, A
	31	78.6	1.1	191569	3	US-09-949-016-15940	Sequence 15940, A
c	32	78.2	1.1	50000	3	US-09-662-254B-23	Sequence 23, Appl
	33	77.4	1.1	19124	2	US-08-487-826B-13	Sequence 13, Appl
	34	76.8	1.1	50000	3	US-09-662-254B-23	Sequence 23, Appl
	35	76.6	1.1	601	3	US-09-949-016-30531	Sequence 30531, A
	36	76.6	1.1	601	3	US-09-949-016-37150	Sequence 37150, A
	37	76.6	1.1	601	3	US-09-949-016-37164	Sequence 37164, A
	38	76.6	1.1	601	3	US-09-949-016-145868	Sequence 145868,
	39	76.6	1.1	601	3	US-09-949-016-146136	Sequence 146136,
	40	76.6	1.1	601	3	US-09-949-016-146404	Sequence 146404,
	41	76.4	1.1	205044	3	US-09-949-016-15851	Sequence 15851, A
	42	76.4	1.1	205044	3	US-09-949-016-15852	Sequence 15852, A
	43	76.4	1.1	205044	3	US-09-949-016-15853	Sequence 15853, A
	44	76.4	1.1	223471	3	US-09-949-016-12387	Sequence 12387, A
	45	76.4	1.1	223471	3	US-09-949-016-12724	Sequence 12724, A

ALIGNMENTS

RESULT 1

US-09-502-426B-1

; Sequence 1, Application US/09502426B

; Patent No. 6987025

; GENERAL INFORMATION:

; APPLICANT: Azpiroz, Ricardo

; APPLICANT: Choe, Sunghwa

; APPLICANT: Feldmann, Kenneth A.

; TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF

; FILE REFERENCE: 11696-070001

; CURRENT APPLICATION NUMBER: US/09/502,426B

; CURRENT FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: US 60/119,657

; PRIOR FILING DATE: 1999-02-11

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 1, 2006, 05:56:48 ; Search time 5055 Seconds
 (without alignments)
 16743.270 Million cell updates/sec

Title: US-10-804-772-1
 Perfect score: 6888
 Sequence: 1 atgtgggtattatattgttg.....cctagttcaggccaaagctt 6888

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	6888	100.0	6888	9	US-10-804-772-1	Sequence 1, Appli

	2	3379	49.1	3379	16	US-11-112-824-19	Sequence 19, Appl
	3	669	9.7	1035	16	US-11-112-824-4	Sequence 4, Appli
	4	181.8	2.6	1002	8	US-10-424-599-139902	Sequence 139902,
c	5	140.4	2.0	8056	9	US-10-473-126-386	Sequence 386, App
	6	136.4	2.0	8056	9	US-10-473-126-386	Sequence 386, App
	7	135.6	2.0	6508	3	US-09-995-917A-2	Sequence 2, Appli
	8	132.8	1.9	1509	16	US-11-112-824-21	Sequence 21, Appl
	9	132.8	1.9	1511	8	US-10-437-963-87405	Sequence 87405, A
	10	132.8	1.9	1521	8	US-10-395-463-1	Sequence 1, Appli
	11	127.8	1.9	2066	8	US-10-425-114-35701	Sequence 35701, A
c	12	124	1.8	8056	9	US-10-473-126-240	Sequence 240, App
	13	123.2	1.8	8056	9	US-10-473-126-240	Sequence 240, App
	14	112.4	1.6	1013	9	US-10-425-115-12401	Sequence 12401, A
	15	105.4	1.5	837	8	US-10-424-599-68299	Sequence 68299, A
	16	103	1.5	3673778	7	US-10-312-841-1	Sequence 1, Appli
c	17	100.2	1.5	3673778	7	US-10-312-841-1	Sequence 1, Appli
	18	94.8	1.4	171486	15	US-11-121-086-105	Sequence 105, App
c	19	94.8	1.4	171486	15	US-11-121-086-105	Sequence 105, App
	20	93.2	1.4	49979	8	US-10-741-601-5746	Sequence 5746, Ap
	21	93.2	1.4	49979	9	US-10-741-600-17905	Sequence 17905, A
	22	92.4	1.3	49979	10	US-10-995-561-13443	Sequence 13443, A
c	23	91.6	1.3	960	6	US-10-198-846-6381	Sequence 6381, Ap
	24	89.8	1.3	115218	9	US-10-278-698-255	Sequence 255, App
	25	89.8	1.3	115218	9	US-10-278-698-769	Sequence 769, App
	26	87.6	1.3	568	3	US-09-770-152-316	Sequence 316, App
	27	87.6	1.3	1419	3	US-09-938-842A-619	Sequence 619, App
	28	87.6	1.3	1419	3	US-09-938-842A-619	Sequence 619, App
	29	87.6	1.3	1649	16	US-11-172-740-2328	Sequence 2328, Ap
	30	87.6	1.3	1682	16	US-11-208-308-1	Sequence 1, Appli
c	31	87.4	1.3	158001	8	US-10-211-179-11	GENERAL INFORMATI
	32	87	1.3	173602	15	US-11-121-086-25	Sequence 25, Appl
c	33	86.8	1.3	755	6	US-10-027-632-128109	Sequence 128109,
c	34	86.8	1.3	755	7	US-10-027-632-128109	Sequence 128109,
c	35	86.4	1.3	38678	10	US-10-893-315-136	Sequence 136, App
c	36	86.4	1.3	38684	10	US-10-893-315-154	Sequence 154, App
	37	86.4	1.3	158001	8	US-10-211-179-11	GENERAL INFORMATI
	38	84.6	1.2	9810	7	US-10-311-455-400	Sequence 400, App
	39	84.2	1.2	26772	10	US-10-995-561-13313	Sequence 13313, A
	40	84.2	1.2	54946	10	US-10-995-561-13479	Sequence 13479, A
c	41	83.8	1.2	8170	7	US-10-240-453-131	Sequence 131, App
	42	82.8	1.2	6131	7	US-10-311-455-863	Sequence 863, App
	43	82.6	1.2	9810	7	US-10-311-455-399	Sequence 399, App
c	44	82.6	1.2	15732	6	US-10-239-676-95	Sequence 95, Appl
c	45	82.6	1.2	15732	7	US-10-240-453-107	Sequence 107, App

ALIGNMENTS

RESULT 1

US-10-804-772-1

; Sequence 1, Application US/10804772

; Publication No. US20040244077A1

; GENERAL INFORMATION:

; APPLICANT: Azpiroz, Ricardo

; APPLICANT: Choe, Sunghwa

; APPLICANT: Feldmann, Kenneth A.